

SEQUENCE LISTING

<110> Hoechst Schering AgrEvo GmbH
 <120> Nucleic acid molecules encoding wheat enzymes
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 <151> 1998-05-08
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GCGCGCCCCG CGGCAGCAGC AGCACCAGCAG TGGGAGAGAG AGGCTTCGCC CCGGCCCCGA	206
CCGAGCGGGG CGATCCACCG TCCGTGCGTC CGCACMCCT CCGCCTCCTC CCCTGTCCCG	366
CGCGCCCA CAC ATG GCG GCG ACG GGC GTC GGC GCC GGG TGC CTC GCC	315
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1 5 10	
CCC AGC GTC CGC CTG CGC GCC GAT CCG GCG ACG GCG GCC CGG GCG TCC	363
Pro Ser Val Arg Leu Arg Ala Asp Pro Ala Thr Ala Ala Arg Ala Ser	
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GCC TGC GTC GTC CGC GCG CGG CTC CGG CGC TTG GCG CGG GGC CGC TAC	411
Ala Cys Val Val Arg Ala Arg Leu Arg Arg Leu Ala Arg Gly Arg Tyr	
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GTC GCC GAG CTC AGC AGG GAG GGC CCC GCG GCG CGC CCC GCG CAG CAG	459
Val Ala Glu Leu Ser Arg Glu Gly Pro Ala Ala Arg Pro Ala Gln Gln	
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CAG CAA CTG GCC CCG CCG CTC GTG CCA GGC TTC CTC GCG CCG CCG CCG	507
Gln Gln Leu Ala Pro Pro Leu Val Pro Gly Phe Leu Ala Pro Pro Pro	
65 70 75	
CCC GCG CCC GCC CAG TCG CCG GCC CCG ACG CAG CCG CCC CTC CCG GAC	555
Pro Ala Pro Ala Gln Ser Pro Ala Pro Thr Gln Pro Pro Leu Pro Asp	
80 85 90	

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GCC GGC GTG GGG GAA CTC GCG CCC GAC CTC CTG CTC GAA GGG ATT GCT 603
 Ala Gly Val Gly Leu Ala Pro Asp Leu Leu Leu Glu Gly Ile Ala
 95 100 105

GAG GAT TCC ATC GAC AGC ATA ATT GTG GCT GCA AGT GAG CAG GAT TCT 651
 Glu Asp Ser Ile Asp Ser Ile Ile Val Ala Ala Ser Glu Gln Asp Ser
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GAG ATC ATG GAT GCG AAT GAG CAA CCT CAA GCT AAA GTT ACA CGT AGC 699
 Glu Ile Met Asp Ala Asn Glu Gln Pro Gln Ala Lys Val Thr Arg Ser
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ATC GTG TTT GTG ACT GGT GAA GCT GCT CCT TAT GCA AAG TCA GGG GGG 747
 Ile Val Phe Val Thr Gly Glu Ala Ala Pro Tyr Ala Lys Ser Gly Gly
 145 150 155

TTG GGA GAT GTT TGT GGT TCG TTA CCA ATT GCT CTT GCT GCT CGT GGT 795
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 160 165 170

CAC CGA GTG ATG GTT GTA ATG CCA AGA TAC TTA AAT GGG TCC TCT GAT 843
 His Arg Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Ser Ser Asp
 175 180 185

AAA AAC TAT GCA AAG GCA TTA TAC ACT GCG AAG CAC ATT AAG ATT CCA 891
 Lys Asn Tyr Ala Lys Ala Leu Tyr Thr Ala Lys His Ile Lys Ile Pro
 190 195 200

TGC TTT GGG GGA TCA CAT GAA GTG ACC TTT TTT CAT GAG TAT AGA GAC 939
 Cys Phe Gly Gly Ser His Glu Val Thr Phe Phe His Glu Tyr Arg Asp
 205 210 215 220

AAC GTC GAT TGG GTG TTT GTC GAT CAT CCG TCA TAT CAC AGA CCA GGA 987
 Asn Val Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly
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AGT TTA TAT GGA GAT AAT TTT GGT GCT TTT GGT GAT AAT CAG TTC AGA 1035
 Ser Leu Tyr Gly Asp Asn Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg
 240 245 250

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 Trp His Ala Ser Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro
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GTC GAT GAC CTC TCT GGA AAG GCC AAA TGT AAA GCT GAA TTG CAG AAG Val Asp Asp Leu Ser Gly Lys Ala Lys Cys Lys Ala Glu Leu Gln Lys 430 435 440	1611
GAG TTG GGT TTA CCT GTA AGG GAG GAT GTT CCT CTG ATT GGC TTT ATT Glu Leu Gly Leu Pro Val Arg Glu Asp Val Pro Leu Ile Gly Phe Ile 445 450 455 460	1659
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CCA GAG CTC ATG AGG GAG GAC GTG CAA TTT GTC ATG CTT GGA TCT GGG Pro Glu Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly 480 485 490	1755
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Asp Lys Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg	
510 515 520	
ATA ACT GCA GGT TGC GAT ATA TTG TTA ATG CCA TCG AGA TTT GAA CCT	1899
Ile Thr Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro	
525 530 535 540	
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Cys Gly Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val	
545 550 555	
GTT CAT GGA ACT GGG GGC CTC CGA GAC ACA GTC GAG ACC TTC AAC CCT	1995
Val His Gly Thr Gly Gly Leu Arg Asp Thr Val Glu Thr Phe Asn Pro	
560 565 570	
TTT GGT GCA AAA GGA GAG GAG GGT ACA GGG TGG GCG TTC TCA CCG CTA	2043
Phe Gly Ala Lys Gly Glu Glu Gly Thr Gly Trp Ala Phe Ser Pro Leu	
575 580 585	
ACC GTG GAC AAG ATG TTG TGG GCA TTG CGA ACC GCG ATG TCG ACA TTC	2091
Thr Val Asp Lys Met Leu Trp Ala Leu Arg Thr Ala Met Ser Thr Phe	
590 595 600	
AGG GAG CAC AAG CCG TCC TGG GAG GGG CTC ATG AAG CGA GGC ATG ACG	2139
Arg Glu His Lys Pro Ser Trp Glu Gly Leu Met Lys Arg Gly Met Thr	
605 610 615 620	
AAA GAC CAT ACG TGG GAC CAT GCC CCG AGC AGT ACG AGC AGA TCT TCG	2187
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625 630 635	
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640 645 650	
AGG TCC AAG TGC GAG TCT CCT TCA GCT CTG AAG ACA TCC TCT TCA TCC	2283
Arg Ser Lys Cys Glu Ser Pro Ser Ala Leu Lys Thr Ser Ser Ser Ser	
655 660 665	
TTC CGC GGC CCG GAA GGA TAC CCC TGT ACA TTG CGT TGT CCT GCT ACA	2331
Phe Arg Gly Pro Glu Gly Tyr Pro Cys Thr Leu Arg Cys Pro Ala Thr	
670 675 680	
GTA GAG TCG CAA TGC GCC TGC TTG CTT TGG TTC GCC GGT TCG AGA ACA	2379
Val Glu Ser Gln Cys Ala Cys Leu Leu Trp Phe Ala Gly Ser Arg Thr	
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Tyr Asp Gly Cys Ala Ala Ala Val Thr Ala Ser Gly Gly Arg Gln	
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 Leu Gln Phe Trp Gly Ile Arg Lys Gly Cys Ala Ala Gly Trp Leu Thr
 720 725 730

GCA AAG CAC CAC TCA GAT GGC AGC CTC TCT GTC CGT GTT ACA GCT GAA 2523
 Ala Lys His His Ser Asp Gly Ser Leu Ser Val Arg Val Thr Ala Glu
 735 740 745

ATC AGA AAC CAA CTG GTG ACT CTT TAGCCTTAGT GATTGTGAAG TTTGTTGCCT 2577
 Ile Arg Asn Gln Leu Val Thr Leu
 750 755

TCTGTGTATG TTGTCTTGTC CTTAGCTGAC AAATATTTGA CCTGTTGGAG AATTTTATCT 2637

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Arg Ala Arg Leu Arg Arg Leu Ala Arg Gly Arg Tyr Val Ala Glu Leu
 35 40 45

Ser Arg Glu Gly Pro Ala Ala Arg Pro Ala Gln Gln Gln Gln Leu Ala
 50 55 60

Pro Pro Leu Val Pro Gly Phe Leu Ala Pro Pro Pro Pro Ala Pro Ala
 65 70 75 80

Gln Ser Pro Ala Pro Thr Gln Pro Pro Leu Pro Asp Ala Gly Val Gly
 85 90 95

Glu Leu Ala Pro Asp Leu Leu Leu Glu Gly Ile Ala Glu Asp Ser Ile
 100 105 110

Asp Ser Ile Ile Val Ala Ala Ser Glu Gln Asp Ser Glu Ile Met Asp
 115 120 125

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Ala Asn Glu Gln Pro Gln Ala Lys Val Thr Arg Ser Ile Val Phe Val
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 Thr Gly Glu Ala Ala Pro Tyr Ala Lys Ser Gly Gly Leu Gly Asp Val
 145 150 155 160
 Cys Gly Ser Leu Pro Ile Ala Leu Ala Ala Arg Gly His Arg Val Met
 165 170 175
 Val Val Met Pro Arg Tyr Leu Asn Gly Ser Ser Asp Lys Asn Tyr Ala
 180 185 190
 Lys Ala Leu Tyr Thr Ala Lys His Ile Lys Ile Pro Cys Phe Gly Gly
 195 200 205
 Ser His Glu Val Thr Phe Phe His Glu Tyr Arg Asp Asn Val Asp Trp
 210 215 220
 Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly Ser Leu Tyr Gly
 225 230 235 240
 Asp Asn Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg Tyr Thr Leu Leu
 245 250 255
 Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile Leu Glu Leu Gly Gly Tyr
 260 265 270
 Ile Tyr Gly Gln Asn Cys Met Phe Val Val Asn Asp Trp His Ala Ser
 275 280 285
 Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro Tyr Gly Val Tyr
 290 295 300
 Arg Asp Ser Arg Ser Thr Leu Val Ile His Asn Leu Ala His Gln Gly
 305 310 315 320
 Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro Glu Trp
 325 330 335
 Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg His Ala
 340 345 350
 Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val Val Thr
 355 360 365
 Ala Asp Arg Ile Val Thr Val Ser Gln Gly Tyr Ser Trp Glu Val Thr
 370 375 380
 Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser Arg Lys
 385 390 395 400
 Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp Trp Asn
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 Ser Gly Lys Ala Lys Cys Lys Ala Glu Leu Gln Lys Glu Leu Gly Leu
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 Pro Val Arg Glu Asp Val Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp
 450 455 460
 Tyr Gln Lys Gly Ile Asp Leu Ile Lys Met Ala Ile Pro Glu Leu Met
 465 470 475 480
 Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro Ile Phe
 485 490 495
 Glu Gly Trp Met Arg Ser Thr Glu Ser Ser Tyr Lys Asp Lys Phe Arg
 500 505 510
 Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr Ala Gly
 515 520 525
 Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn
 530 535 540
 Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His Gly Thr
 545 550 555 560
 Gly Gly Leu Arg Asp Thr Val Glu Thr Phe Asn Pro Phe Gly Ala Lys
 565 570 575
 Gly Glu Glu Gly Thr Gly Trp Ala Phe Ser Pro Leu Thr Val Asp Lys
 580 585 590
 Met Leu Trp Ala Leu Arg Thr Ala Met Ser Thr Phe Arg Glu His Lys
 595 600 605
 Pro Ser Trp Glu Gly Leu Met Lys Arg Gly Met Thr Lys Asp His Thr
 610 615 620
 Trp Asp His Ala Pro Ser Ser Thr Ser Arg Ser Ser Ser Gly Pro Ser
 625 630 635 640
 Trp Thr Asn Pro Thr Ser Cys Arg Arg Gly Leu Gly Arg Ser Lys Cys
 645 650 655
 Glu Ser Pro Ser Ala Leu Lys Thr Ser Ser Ser Ser Phe Arg Gly Pro
 660 665 670
 Glu Gly Tyr Pro Cys Thr Leu Arg Cys Pro Ala Thr Val Glu Ser Gln
 675 680 685
 Cys Ala Cys Leu Leu Trp Phe Ala Gly Ser Arg Thr Tyr Asp Gly Cys
 690 695 700

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Ala Ala Ala Ala Val Thr Ala Ser Gly Gly Arg Gln Leu Gln Phe Trp
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Gly Ile Arg Lys Gly Cys Ala Ala Gly Trp Leu Thr Ala Lys His His
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